The following Listing of the Claims will replace all prior versions and all prior listings of the claims in the present application:

Listing of The Claims:

1. (Currently amended) A method for preparing a cell line ~~capable of~~ exhibiting directed constitutive hypermutation of a target nucleic acid region, comprising screening a cell population for ongoing target sequence diversification, wherein said screening comprises determining the mutation rate of the target nucleic acid region relative to the mutation rate of a non-target nucleic acid region, and selecting a cell in which the rate of target nucleic acid mutation exceeds that of ~~other nucleic acid mutation~~ non-target nucleic acid region by a factor of 100 or more, wherein the rate of mutation in the cell is modulated by genetic manipulation, wherein said genetic manipulation is selected from the group consisting of gene deletion, conversion, and insertion.

2. (Original) A method according to claim 1, wherein the cell line is a lymphoid cell line.

3. (Currently amended) A method according to claim 2, wherein the cell line is ~~derived from~~ an immunoglobulin-expressing cell.

4. (Original)A method according to claim 1, wherein the cell line expresses the target nucleic acid region in a manner that facilitates selection of cells comprising mutants of said region.

5. (Currently Amended) A method according to claim 4, wherein the cell line expresses ~~the~~ a gene product encoded by the target nucleic acid region on the cell surface.

6. (Currently amended) A method according to claim 1, wherein the cell line ~~is derived from or related to~~ comprises a cell type which hypermutates *in vivo*.

7. (Original) A method according to claim 6, wherein the cell line is a Burkitt lymphoma, follicular lymphoma or diffuse large cell lymphoma cell line.

8. (Original) A method according to claim 1, further comprising the steps of isolating one or more cells which display target sequence diversification, and comparing the rate of accumulation of mutations in the target sequences with that in non-target sequences in the isolated cells.

9. (Original) A method according to claim 8, wherein the target sequence is an immunoglobulin V-gene sequence.

10. (Currently amended) A method according to claim 9, wherein ~~the~~ cells of said cell population are screened by assessing loss of an expressed immunoglobulin.

11. (Currently amended) A method according to claim 1 or 8, wherein ~~the~~ cells of said cell population are screened by assessment of mutation rates by direct sequencing of the target sequences.

12. (Currently amended) A method according to claim 1 or 8, wherein ~~the~~ cells of said cell population are screened by an immunofluorescence technique.

13. (Cancelled)

14. (Currently amended) A method according to claim 1, wherein one or more ~~genes involved in~~ DNA repair genes are manipulated.

15. (Original)A method according to claim 14, wherein said one or more genes are Rad51 analogues and/or paralogues.

16. (Original)A method according to claim 14, wherein the genes are selected from the group consisting of Rad51b, Rad51c and analogues and/or paralogues thereof.